

Supplementary Figure Legends

Supplementary Figure 1. Log likelihood scores. X-axis indicates K values 2 to 18.

Supplementary Figure 2. Cross-validation indexes for K=2-18. X-axis indicates K values 2 to 18.

Supplementary Figure 3. Y chromosomal haplogroup frequencies and diversity values in Ami and Yami.

Supplementary Figure 4A. Y-SNP PCA plot based of Ami, Yami and reference populations. Please refer to Supplementary Table 1 for specific populations examined.

Supplementary Figure 4B. Y-SNP PCA plot based of Ami, Yami and reference groups of populations. Please refer to Supplementary Table 1 for specific populations examined within each region.

Supplementary Figure 5A. MtDNA PCA plot based of Ami, Yami and reference populations. Please refer to Supplementary Table 1 for specific populations examined.

Supplementary Figure 5B. MtDNA PCA plot based of Ami, Yami and reference groups of populations. Please refer to Supplementary Table 1 for specific populations examined within each region.

Supplementary Figure 6. Phylogenetic tree based on complete mtDNA sequences of B4a/B4g suprahaplogroup in Ami, Yami and Society Islands of French Polynesia. Numbers indicate mutations and positions. Designations in color indicate samples.

Supplementary Figure 7. Phylogenetic tree based on complete mtDNA sequences of B4 suprahaplogroup in Ami, Yami and Society Islands of French Polynesia. Numbers indicate mutations and positions. Designations in color indicate samples.

Supplementary Figure 8. Phylogenetic tree based on complete mtDNA sequences of B4c suprahaplogroup in Ami, Yami and Society Islands of French Polynesia. Numbers indicate mutations and positions. Designations in color indicate samples.

Supplementary Figure 9. Phylogenetic tree based on complete mtDNA sequences of B5 suprahaplogroup in Ami, Yami and Society Islands of French Polynesia. Numbers indicate mutations and positions. Designations in color indicate samples.

Supplementary Figure 10. Phylogenetic tree based on complete mtDNA sequences of F1 suprahaplogroup in Ami, Yami and Society Islands of French Polynesia. Numbers indicate mutations and positions. Designations in color indicate samples.

Supplementary Figure 11. Phylogenetic tree based on complete mtDNA sequences of F4/F3 suprahaplogroup in Ami, Yami and Society Islands of French Polynesia. Numbers indicate mutations and positions. Designations in color indicate samples.

Supplementary Figure 12. Ami BSP plot.

Supplementary Figure 13. Yami BSP plot.

Supplementary Figure 14A. PC1/PC2 plot based on autosomal SNP loci. Key to the populations examined is provided in the upper right-hand corner of the graph. Please refer to Supplementary Table 1 for specific populations examined within each region.

Supplementary Figure 14B. Expansion of PC1/PC2 plot based on autosomal SNP loci. Key to the populations examined is provided in the upper right-hand corner of Figure 1A. Please refer to Supplementary Table 1 for specific populations examined within each region.

Supplementary Figure 15A. PC1/PC3 plot based on autosomal SNP loci. Key to the populations examined is provided in the lower right-hand corner of the graph. Please refer to Supplementary Table 1 for specific populations examined within each region.

Supplementary Figure 15B. Expansion of PC1/PC3 plot based on autosomal SNP loci. Key to the populations examined is provided in the lower right-hand corner of Figure 2A. Please refer to Supplementary Table 1 for specific populations examined within each region.

Supplementary Figure 16A. Identical by descent tracts (IBDs) of populations relative to the Ami. Please refer to Supplementary Table 1 for specific populations examined within each region. Box on the lower left-hand corner indicates size range of tracts. Y-axis provides the median IBD counts and 95% CI (confidence intervals).

Supplementary Figure 16B. Identical by descent tracts (IBDs) of populations relative to the Yami. Supplementary Table 1 for specific populations examined within each region. Box on the lower left-hand corner indicates size range of tracts. Y-axis provides the median IBD counts and 95% CI (confidence intervals).

Supplementary Figure 17. Ami IBD total length.

Supplementary Figure 18. Yami IBD total length.

Supplementary Tables

Supplementary Table 1. Populations analyzed.

Supplementary Table 2. New Y-SNP Ami and Yami primer specifications.

Supplementary Table 3. Ami haplogroups and genotypes.

Supplementary Table 4. Yami haplogroups and genotypes.

Supplementary Table 5. Y chromosome haplogroup frequencies used for PCA.

Supplementary Table 6 Ami and Yami mtDNA frequencies.

Supplementary Table 7. Supplementary Table 7. mtDNA genotype data and the assigned haplogroup of every individual.

Supplementary Table 8. Mitochondrial DNA haplogroup frequencies used for PCA.

Supplementary Table 9 Ami Admixture f3 values.

Supplementary Table 10. Yami Admixture f3 values.

Supplementary Table 11. Ami and Yami Admixture f4

Supplementary Table 12. Ami Outgroup values.

Supplementary Table 13. Yami Outgroup values.

Supplementary Table 14. Ami and Yami heterozygosity values.

Supplementary Table 15. IBD Average Lengths sharing with Ami and Yami.

Supplementary Table 16. T-test results comparing the Manhattan distances of Ami and Yami to MSEA and ISEA populations based on Y chromosome markers of every population.

Supplementary Table 17. T-test results comparing the Manhattan distances of Ami and Yami to MSEA and ISEA populations based on Y chromosome markers of population groups.

Supplementary Table 18. T-test results comparing the Manhattan distances of Ami and Yami to MSEA and ISEA populations based on mtDNA of every population.

Supplementary Table 19. T-test results comparing the Manhattan distances of Ami and Yami to MSEA and ISEA populations based on mtDNA of population groups.

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11